

AMENDMENTS TO THE SPECIFICATIONIN THE WRITTEN DESCRIPTION:

Please replace the paragraph starting at page 3, line 3  
with the following amended paragraph.

The present invention also provides SEQ ID NO: 2, which is a novel trehalose synthase protein with the following amino acid sequence:

Met	Ser	Ile	Pro	Asp	Asn	Thr	Tyr	Ile	Glu	Trp	Leu	Val	Ser	Gln
				5					10					15
Ser	Met	Leu	His	Ala	Ala	Arg	Glu	Arg	Ser	Arg	His	Tyr	Ala	Gly
				20					25					30
Gln	Ala	Arg	Leu	Trp	Gln	Arg	Pro	Try	Ala	Gln	Ala	Arg	Pro	Arg
				35					40					45
Asp	Ala	Ser	Ala	Ile	Ala	Ser	Val	Trp	Phe	Thr	Ala	Tyr	Pro	Ala
				50					55					60
Ala	Ile	Ile	Thr	Pro	Glu	Gly	Gly	Thr	Val	Leu	Glu	Ala	Leu	Gly
				65					70					75
Asp	Asp	Arg	Leu	Trp	Ser	Ala	Leu	Ser	Glu	Leu	Gly	Val	Gln	Gly
				80					85					90
Ile	His	Asn	Gly	Pro	Met	Lys	Arg	Ser	Gly	Gly	Leu	Arg	Gly	Arg
				95					100					105
Glu	Phe	Thr	Pro	Thr	Ile	Asp	Gly	Asn	Phe	Asp	Arg	Ile	Ser	Phe
				110					115					120
Asp	Ile	Asp	Pro	Ser	Leu	Gly	Thr	Glu	Glu	Gln	Met	Leu	Gln	Leu
				125					130					135
Ser	Arg	Val	Ala	Ala	Ala	His	Asn	Ala	Ile	Val	Ile	Asp	Asp	Ile
				140					145					150

Val	Pro	Ala	His	Thr	Gly	Lys	Gly	Ala	Asp	Phe	Arg	Leu	Ala	Glu
				155					160					165
Met	Ala	Tyr	Gly	Asp	Tyr	Pro	Gly	Leu	Tyr	His	Met	Val	Glu	Ile
				170					175					180
Arg	Glu	Glu	Asp	Trp	Glu	Leu	Leu	Pro	Glu	Val	Pro	Ala	Gly	Arg
				185					190					195
Asp	Ser	Val	Asn	Leu	Leu	Pro	Pro	Val	Val	Asp	Arg	Leu	Lys	Glu
				200					205					210
Lys	His	Tyr	Ile	Val	Gly	Gln	Leu	Gln	Arg	Val	Ile	Phe	Phe	Glu
				215					220					225
Pro	Gly	Ile	Lys	Asp	Thr	Asp	Trp	Ser	Val	Thr	Gly	Glu	Val	Thr
				230					235					240
Gly	Val	Asp	Gly	Lys	Val	Arg	Arg	Trp	Val	Tyr	Leu	His	Tyr	Phe
				245					250					255
Lys	Glu	Gly	Gln	Pro	Ser	Lue	Asn	Trp	Leu	Asp	Pro	Thr	Phe	Ala
				260					265					270
Ala	Gln	Gln	Leu	Ile	Ile	Gly	Asp	Ala	Leu	His	Ala	Ile	Asp	Val
				275					280					285
Thr	Gly	Ala	Arg	Val	Leu	Arg	Leu	Asp	Ala	Asn	Gly	Phe	Leu	Gly
				290					295					300
Val	Glu	Arg	Arg	Ala	Glu	Gly	Thr	Ala	Trp	Ser	Glu	Gly	His	Pro
				305					310					315
Leu	Ser	Val	Thr	Gly	Asn	Gln	Leu	Leu	Ala	Gly	Ala	Ile	Arg	Lys
				320					325					330
Ala	Gly	Gly	Phe	Ser	Phe	Gln	Glu	Leu	Asn	Leu	Thr	Ile	Asp	Asp
				335					340					345
Ile	Ala	Ala	Met	Ser	His	Gly	Gly	Ala	Asp	Leu	Ser	Tyr	Asp	Phe
				350					355					360

Ile	Thr	Arg	Pro	Ala	Tyr	His	His	Ala	Leu	Leu	Thr	Gly	Asp	Thr
				365					370					375
Glu	Phe	Leu	Arg	Met	Met	Leu	Arg	Glu	Val	His	Ala	Phe	Gly	Ile
				380					385					390
Asp	Pro	Ala	Ser	Leu	Ile	His	Ala	Leu	Gln	Asn	His	Asp	Glu	Leu
				395					400					405
Thr	Leu	Glu	Leu	Val	His	Phe	Trp	Thr	Leu	His	Ala	Tyr	Asp	His
				410					415					420
Tyr	His	Tyr	Lys	Gly	Gln	Thr	Leu	Pro	Gly	Gly	His	Leu	Arg	Glu
				425					430					435
His	Ile	Arg	Glu	Glu	Met	Tyr	Glu	Arg	Leu	Thr	Gly	Glu	His	Ala
				440					445					450
Pro	Tyr	Asn	Leu	Lys	Phe	Val	Thr	Asn	Gly	Val	Ser	Cys	Thr	Thr
				455					460					465
Ala	Ser	Val	Ile	Ala	Ala	Ala	Leu	Asn	Ile	Arg	Asp	Leu	Asp	Ala
				470					475					480
Ile	Gly	Pro	Ala	Glu	Val	Glu	Gln	Ile	Gln	Arg	Leu	His	Ile	Leu
				485					490					495
Leu	Val	Met	Phe	Asn	Ala	Met	Gln	Pro	Gly	Val	Phe	Ala	Leu	Ser
				500					505					510
Gly	Trp	Asp	Leu	Val	Gly	Ala	Leu	Pro	Leu	Ala	Pro	Glu	Gln	Val
				515					520					525
Glu	His	Leu	Met	Gly	Asp	Gly	Asp	Thr	Arg	Trp	Ile	Asn	Arg	Gly
				530					535					540
Gly	Tyr	Asp	Leu	Ala	Asp	Leu	Ala	Pro	Glu	Ala	Ser	Val	Ser	Ala
				545					550					555
Glu	Gly	Leu	Pro	Lys	Ala	Arg	Ser	Leu	Tyr	Gly	Ser	Leu	Ala	Glu
				560					565					570

Gln	Leu	Gln	Arg	Pro	Gly	Ser	Phe	Ala	Cys	Gln	Leu	Lys	Arg	Ile
				575					580					585
Leu	Ser	Val	Arg	Gln	Ala	Tyr	Asp	Ile	Ala	Ala	Ser	Lys	Gln	Ile
				590					595					600
Leu	Ile	Pro	Asp	Val	Gln	Ala	Pro	Gly	Leu	Leu	Val	Met	Val	His
				605					610					615
Glu	Leu	Pro	Ala	Gly	Lys	Gly	Val	Gln	Leu	Thr	Ala	Leu	Asn	Phe
				620					625					630
Ser	Ala	Glu	Pro	Val	Ser	Glu	Thr	Ile	Cys	Leu	Pro	Gly	Val	Ala
				635					640					645
Pro	Gly	Pro	Val	Val	Asp	Ile	Ile	His	Glu	Ser	Val	Glu	Gly	Asp
				650					655					660
Leu	Thr	Asp	Asn	Cys	Glu	Leu	Gln	Ile	Asn	Leu	Asp	Pro	Tyr	Glu
				665					670					675
Gly	Leu	Ala	Leu	Arg	Val	Val	Ser	Ala	Ala	Pro	Pro	Val	Ile.	
				680					685					

Please replace the paragraph starting at page 6, line 1  
with the following amended paragraph.

In addition, the present invention provides SEQ ID NO: 1,  
which is a novel trehalose synthase gene with the following  
nucleotide sequence:

GATCGCTGGC	GTACTGCAGG	TAGAGCAGGC	GCATCGGCC	CCAGGGCGCA	TCGGCCGGCT	60
CCGCTGTGCC	CTGCTGGTTC	ATGAAGCGGA	CGAACGGGCC	ATCGCGGAAC	CGTGGACGCC	120
ATTCGGGGCT	GTCCGGGTCG	CGGCTGTCGG	TGAGCGTGC	CCACAGGTCG	CTGCGAAACG	180
GCGGACCGCT	CCAAAGCGCG	CCGTGGATGG	GATGCCGAG	CAGTTCGTGC	AGCTCCCAGG	240
AACGTTGCGA	ATGCAGCGCG	CCGAGGCTCA	GGCCATGCAG	ATACAGGCGC	GGTCGGCGTT	300
CGGCCGGCAG	TTCGGTCCAG	TAGCCATAGA	TCTCGGCGAA	TAGCGCGCG	GCCACGTCGC	360

GGCCGTAGTC	GGCCTCCACC	AGCAGCGCCA	GCGGCTGTT	CAGATAGGAG	TACTGCAACG	420
CCACGCTGGC	GATATCGCCG	TGGTGCAGGT	ATTCCACTGC	GTTCATCGCC	GCCGGGTCGA	480
TCCAGCCGGT	ACCGGTGGC	GTCACCAGCA	CCAGCACCGA	TCGCTCGAAG	GCGCCGCTGC	540
GCTGCAGCTC	GCGCAAGGCC	AGACGCGCCC	GCTGGCGCGG	GGTCTCTGCC	GCGCGCAGAC	600
CGACGTAGAC	GCGAATCGGC	TCGAGCGCCG	AGCGGCCGCT	CAAGACGCTG	ATATCCGCCG	660
CCGACGGGCC	GGAGCCGATG	AACTCGCGGC	CGGTGCGGCC	CAGCTCCTCC	CAGCGCAGCA	720
ACGAGGCCCG	GCTGCCGCTT	TTCAGCGCGG	AGGCCGGTGG	CGCCGTCTCC	GGTCGATCA	780
GGGCGTCGTA	CTGCGCGAAG	GATGCGTCCA	GCATGCGCAG	TGCCCCGCC	GCCAGCACAT	840
CGCTGAGCAG	CGACCAGAAC	AGCGCCAGCG	CCACCAGCAC	GCCGATCACG	TTGGCCAGGC	900
GCCGTGGCAG	CACGCCGTCG	GCGTGCCGCG	AGACCGAAGCG	CGACACCAGC	CGATACAGAC	960
GCGCCAGCGT	CAGCAGGATG	AGAAAGGTCG	CCAGCGCGGT	GAGAATGACT	TCGAGCAGGT	1020
GCGCACTGCT	CACCGGCCGC	ATGCCCATCA	GCGCGCGTAC	CGCGTTCTGC	CAGCCGGCGA	1080
CCTGGCTGAG	GAAATAACCG	GCCAGCAGCA	GGCAGCCGAC	CGCGATCAGC	AGATTGACCC	1140
GCTCGCGCTG	CCAGCCTGGG	CGCTCCGGCA	GTTCCAGATA	GCGCCACAGC	CAGGCCAGA	1200
ACACGCCGAG	GCCATAGCCC	ACCGCCAGCG	CCGCGCCGGC	CAGCACGCC	TGGCTCAGCG	1260
TCGAGCGCGG	CAGCAGCGAT	GGCGTCAGCG	CCGCGCAGAA	GAACAGCGTG	CCCAGCAGCA	1320
GGCCGAAACC	GGACAGCGAG	CGCCAGATAT	AGAGGACGGG	CAGGTGCAGC	ATGAAGATCT	1380
CCGGGGTCGG	GTGACGGCGT	CGCGCCTCGG	CATATCGAGG	CGTGTCCGGT	CGTGCAGGTT	1440
CCGTGATGGT	CCGCAGCAGG	CCAATCCGAT	GCAACGATGG	CCGAGCGGCC	GACTCAAACG	1500
TCTACATTTC	CCTAGTGCTG	CCGGAACCGA	TCGCCG			1536

ATG	AGC	ATC	CCA	GAC	AAC	ACC	TAT	ATC	GAA	TGG	CTG	GTC	AGC	CAG	TCC		1584
Met	Ser	Ile	Pro	Asp	Asn	Thr	Tyr	Ile	Glu	Trp	Leu	Val	Ser	Gln	Ser		
ATG	CTG	CAT	GCG	GCC	CGC	GAG	CGG	TCG	CGT	CAT	TAC	GCC	GGC	CAG	GCG		1632
Met	Leu	His	Ala	Ala	Arg	Glu	Arg	Ser	Arg	His	Tyr	Ala	Gly	Gln	Ala		
CGT	CTC	TGG	CAG	CGG	CCT	TAT	GCC	CAG	GCC	CGC	CCG	CGC	GAT	GCC	AGC		1680
Arg	Leu	Trp	Gln	Arg	Pro	Try	Ala	Gln	Ala	Arg	Pro	Arg	Asp	Ala	Ser		
GCC	ATC	GCC	TCG	GTG	TGG	TTC	ACC	GCC	TAT	CCG	GCG	GCC	ATC	ATC	ACG		1728
Ala	Ile	Ala	Ser	Val	Trp	Phe	Thr	Ala	Tyr	Pro	Ala	Ala	Ile	Ile	Thr		
CCG	GAA	GGC	GGC	ACG	GTA	CTC	GAG	GCC	CTC	GGC	GAC	GAC	CGC	CTC	TGG		1776
Pro	Glu	Gly	Gly	Thr	Val	Leu	Glu	Ala	Leu	Gly	Asp	Asp	Arg	Leu	Trp		
AGT	GCG	CTC	TCC	GAA	CTC	GGC	GTG	CAG	GGC	ATC	CAC	AAC	GGG	CCG	ATG		1824
Ser	Ala	Leu	Ser	Glu	Leu	Gly	Val	Gln	Gly	Ile	His	Asn	Gly	Pro	Met		
AAG	CGT	TCC	GGT	GGC	CTG	CGC	GGA	CGC	GAG	TTC	ACC	CCG	ACC	ATC	GAC		1872
Lys	Arg	Ser	Gly	Gly	Leu	Arg	Gly	Arg	Glu	Phe	Thr	Pro	Thr	Ile	Asp		

GGC	AAC	TTC	GAC	CGC	ATC	AGC	TTC	GAT	ATC	GAC	CCG	AGC	CTG	GGG	ACC		1920
Gly	Asn	Phe	Asp	Arg	Ile	Ser	Phe	Asp	Ile	Asp	Pro	Ser	Leu	Gly	Thr		
GAG	GAG	CAG	ATG	CTG	CAG	CTC	AGC	CGG	GTG	GCC	GCG	GCG	CAC	AAC	GCC		1968
Glu	Glu	Gln	Met	Leu	Gln	Leu	Ser	Arg	Val	Ala	Ala	Ala	His	Asn	Ala		
ATC	GTC	ATC	GAC	GAC	ATC	GTG	CCG	GCA	CAC	ACC	GGC	AAG	GGT	GCC	GAC		2016
Ile	Val	Ile	Asp	Asp	Ile	Val	Pro	Ala	His	Thr	Gly	Lys	Gly	Ala	Asp		
TTC	CGC	CTC	GCG	GAA	ATG	GCC	TAT	GGC	GAC	TAC	CCC	GGG	CTG	TAC	CAC		2064
Phe	Arg	Leu	Ala	Glu	Met	Ala	Tyr	Gly	Asp	Tyr	Pro	Gly	Leu	Tyr	His		
ATG	GTG	GAA	ATC	CGC	GAG	GAG	GAC	TGG	GAG	CTG	CTG	CCC	GAG	GTG	CCG		2112
Met	Val	Glu	Ile	Arg	Glu	Glu	Asp	Trp	Glu	Leu	Leu	Pro	Glu	Val	Pro		
GCC	GGG	CGT	GAT	TCG	GTC	AAC	CTG	CTG	CCG	CCG	GTG	GTC	GAC	CGG	CTC		2160
Ala	Gly	Arg	Asp	Ser	Val	Asn	Leu	Leu	Pro	Pro	Val	Val	Asp	Arg	Leu		
AAG	GAA	AAG	CAC	TAC	ATC	GTC	GGC	CAG	CTG	CAG	CGG	GTG	ATC	TTC	TTC		2208
Lys	Glu	Lys	His	Tyr	Ile	Val	Gly	Gln	Leu	Gln	Arg	Val	Ile	Phe	Phe		
GAG	CCG	GGC	ATC	AAG	GAC	ACC	GAC	TGG	AGC	GTC	ACC	GGC	GAG	GTC	ACC		2256
Glu	Pro	Gly	Ile	Lys	Asp	Thr	Asp	Trp	Ser	Val	Thr	Gly	Glu	Val	Thr		
GGG	GTC	GAC	GGC	AAG	GTG	CGT	CGC	TGG	GTC	TAT	CTG	CAC	TAC	TTC	AAG		2304
Gly	Val	Asp	Gly	Lys	Val	Arg	Arg	Trp	Val	Tyr	Leu	His	Tyr	Phe	Lys		
GAG	GGC	CAG	CCG	TCG	CTG	AAC	TGG	CTC	GAC	CCG	ACC	TTC	GCC	GGC	CAG		2352
Glu	Gly	Gln	Pro	Ser	Leu	Asn	Trp	Leu	Asp	Pro	Thr	Phe	Ala	Ala	Gln		
CAG	CTG	ATC	ATC	GGC	GAT	GCG	CTG	CAC	GCC	ATC	GAC	GTC	ACC	GGC	GCC		2400
Gln	Leu	Ile	Ile	Gly	Asp	Ala	Leu	His	Ala	Ile	Asp	Val	Thr	Gly	Ala		
CGG	GTG	CTG	CGC	CTG	GAC	GCC	AAC	GGC	TTC	CTC	GGC	GTG	GAA	CGG	CGC		2448
Arg	Val	Leu	Arg	Leu	Asp	Ala	Asn	Gly	Phe	Leu	Gly	Val	Glu	Arg	Arg		
GCC	GAG	GGC	ACG	GCC	TGG	TCG	GAG	GGC	CAC	CCG	CTG	TCC	GTC	ACC	GGC		2496
Ala	Glu	Gly	Thr	Ala	Trp	Ser	Glu	Gly	His	Pro	Leu	Ser	Val	Thr	Gly		
AAC	CAG	CTG	CTC	GCC	GGG	GCG	ATC	CGC	AAG	GCC	GGC	TTC	AGC	TTC			2544
Asn	Gln	Leu	Leu	Ala	Gly	Ala	Ile	Arg	Lys	Ala	Gly	Gly	Phe	Ser	Phe		
CAG	GAG	CTG	AAC	CTG	ACC	ATC	GAT	GAC	ATC	GCC	ATG	TCC	CAC	GGC		--	2592
Gln	Glu	Leu	Asn	Leu	Thr	Ile	Asp	Asp	Ile	Ala	Ala	Met	Ser	His	Gly	--	
GGG	GCC	GAT	CTG	TCC	TAC	GAC	TTC	ATC	ACC	CGC	CCG	GCC	TAT	CAC	CAT		2640
Gly	Ala	Asp	Leu	Ser	Tyr	Asp	Asp	Phe	Ile	Thr	Arg	Pro	Ala	Tyr	His		
GCG	TTG	CTC	ACC	GGC	GAT	ACC	GAA	TTC	CTG	CGC	ATG	ATG	CTG	CGC	GAA		2688
Ala	Leu	Leu	Thr	Gly	Asp	Thr	Glu	Phe	Leu	Arg	Met	Met	Leu	Arg	Glu		
GTG	CAC	GCC	TTC	GGC	ATC	GAC	CCG	GCG	TCA	CTG	ATC	CAT	GCG	CTG	CAG		2736
Val	His	Ala	Phe	Gly	Ile	Asp	Pro	Ala	Ser	Leu	Ile	His	Ala	Leu	Gln		
AAC	CAT	GAC	GAG	TTC	ACC	CTG	GAG	CTG	GTG	CAC	TTC	TGG	ACG	CTG	CAC		2784
Asn	His	Asp	Glu	Leu	Thr	Leu	Glu	Leu	Val	Phe	Trp	Thr	Leu	His	His		
GCC	TAC	GAC	CAT	TAC	CAC	TAC	AAG	GGC	CAG	ACC	CTG	CCC	GGC	GGC	CAC		2832
Ala	Tyr	Asp	His	Tyr	His	Tyr	Lys	Gly	Gln	Thr	Leu	Pro	Gly	Gly	His		
CTG	CGC	GAA	CAT	ATC	CGC	GAG	GAA	ATG	TAC	GAG	CGG	CTG	ACC	GGC	GAA		2880
Leu	Arg	Glu	His	Ile	Arg	Glu	Glu	Met	Tyr	Glu	Arg	Leu	Thr	Gly	Glu		

CAC	GCG	CCG	TAC	AAC	CTC	AAG	TTC	GTC	ACC	AAC	GGG	GTG	TCC	TGC	ACC		2928
His	Ala	Pro	Tyr	Asn	Leu	Lys	Phe	Val	Thr	Asn	Gly	Val	Ser	Cys	Thr		
ACC	GCC	AGC	GTG	ATC	GCC	GCG	GCG	CTT	AAC	ATC	CGT	GAT	CTG	GAC	GCC		2976
Thr	Ala	Ser	Val	Ile	Ala	Ala	Ala	Leu	Asn	Ile	Arg	Asp	Leu	Asp	Ala		
ATC	GGC	CCG	GCC	GAG	GTG	GAG	CAG	ATC	CAG	CGT	CTG	CAT	ATC	CTG	CTG		3024
Ile	Gly	Pro	Ala	Glu	Val	Glu	Gln	Ile	Gln	Arg	Leu	His	Ile	Leu	Leu		
GTG	ATG	TTC	AAT	GCC	ATG	CAG	CCC	GGC	GTG	TTC	GCC	CTC	TCC	GGC	TGG		3072
Val	Met	Phe	Asn	Ala	Met	Gln	Pro	Gly	Val	Phe	Ala	Leu	Ser	Gly	Trp		
GAT	CTG	GTC	GGC	GCC	CTG	CCG	CTG	GCG	CCC	GAG	CAG	GTC	GAG	CAC	CTG		3120
Asp	Leu	Val	Gly	Ala	Leu	Pro	Leu	Ala	Pro	Glu	Gln	Val	Glu	His	Leu		
ATG	GGC	GAT	GGC	GAT	ACC	CGC	TGG	ATC	AAT	CGC	GGC	GGC	TAT	GAC	CTC		3168
Met	Gly	Asp	Gly	Asp	Thr	Arg	Trp	Ile	Asn	Arg	Gly	Gly	Tyr	Asp	Leu		
GCC	GAT	CTG	GGC	CCG	GAG	GCG	TCG	GTC	TCC	GCC	GAA	GGC	CTG	CCC	AAG		3216
Ala	Asp	Leu	Ala	Pro	Glu	Ala	Ser	Val	Ser	Ala	Glu	Gly	Leu	Pro	Lys		
GCC	CGC	TCG	CTG	TAC	GGC	AGC	CTG	GCC	GAG	CAG	CTG	CAG	CGG	CCA	GGC		3264
Ala	Arg	Ser	Leu	Tyr	Gly	Ser	Leu	Ala	Glu	Gln	Leu	Gln	Arg	Pro	Gly		
TCC	TTC	GCC	TGC	CAG	CTC	AAG	CGC	ATC	CTC	AGC	GTG	CGC	CAG	GCC	TAC		3312
Ser	Phe	Ala	Cys	Gln	Leu	Lys	Arg	Ile	Leu	Ser	Val	Arg	Gln	Ala	Tyr		
GAC	ATC	GCT	GCC	AGC	AAG	CAG	ATC	CTG	ATT	CCG	GAT	GTG	CAG	GGC	CCG		3360
Asp	Ile	Ala	Ala	Ser	Lys	Gln	Ile	Leu	Ile	Pro	Asp	Val	Gln	Ala	Pro		
GGA	CTC	CTG	GTG	ATG	GTC	CAC	GAG	CTG	CCT	GCC	GGC	AAG	GGC	GTG	CAG		3408
Gly	Leu	Leu	Val	Met	Val	His	Glu	Leu	Pro	Ala	Gly	Lys	Gly	Val	Gln		
CTC	ACG	GCA	CTG	AAC	TTC	AGC	GCC	GAG	CCG	GTC	AGC	GAG	ACC	ATC	TGC		3456
Leu	Thr	Ala	Leu	Asn	Phe	Ser	Ala	Glu	Pro	Val	Ser	Glu	Thr	Ile	Cys		
CTG	CCC	GGC	GTG	GCG	CCC	GGC	CCG	GTG	GTG	GAC	ATC	ATT	CAC	GAG	AGT		3504
Leu	Pro	Gly	Val	Ala	Pro	Gly	Pro	Val	Val	Asp	Ile	Ile	His	Glu	Ser		
GTG	GAG	GGC	GAC	CTC	ACC	GAC	AAC	TGC	GAG	CTG	CAG	ATC	AAC	CTC	GAC		3552
Val	Glu	Gly	Asp	Leu	Thr	Asp	Asn	Cys	Glu	Leu	Gln	Ile	Asn	Leu	Asp		
CCG	TAC	GAG	GGG	CTT	GCC	CTG	CGT	GTG	GTG	AGC	GCC	GCG	CCG	CCG	GTG		3600
Pro	Tyr	Glu	Gly	Leu	Ala	Leu	Arg	Val	Val	Ser	Ala	Ala	Pro	Pro	Val		
ATC	TGA	GCGC														3610	
Ile																	
	CCTCTTCGCG	CGCCCCGGGT	CCGCGCTAT	AGTGCGCAGC	GCCTGGGGCG	CGCATTGCC											3670
	TCGCCGTCGA	GACCAGCCCG	TGTCGTTCAC	TTCGCTTTTC	CGCCTTGC	TGCTGCCGCT											3730
	GGCGCTGCTT	GCCGCACCCG	TCTGGCGCA	GACCGCCTGC	CCGCCCGGCC	AGCAGCCGAT											3790
	CTGCCTGAGC	GGCAGCTGCC	TCTGCGTGCC	GGCCGCCGCC	AGCGATCCAC	AGGCGGTCTA											3850
	CGACCGCGTC	CAGCGTATGG	CTACGCTGGC	CCTGCAGAAC	TGGATCCAGC	AGTCGCGCGA											3910
	CCGCCTGATG	GCCGGCGGCG	TCGAGCCGAT	ACCGCTGCAC	ATCCGCTCGC	AGCTCGAGCC											3970
	GTATTCGAT	CTTGCCGTGC	TGGAGAGTGC	GCGGTACCGC	GTCGGCGACG	AGGTGGTGCT											4030
	GACTGCCGGC	AACACCCTGC	TGCGCAACCC	GGACGTCAAT	GCCGTGACCC	TGATCGACGT											4090

CATCGTCTTC	CGCCACGAGG	AGGATGCCCG	GGACAAACGTC	GCGCTCTGGG	CCCATGAGCT	4150
CAAGCACGTC	GAGCAATATC	TGGACTGGGG	CGTCGCCGAG	TTCGCCCGGC	GCTATACGCA	4210
GGATTTCCGT	GCCGTGGAGC	GCCCCGGCCTA	TGCGCTGGAG	CGTGAGGTGG	AAGAGGCCCT	4270
GCGCGAGACG	CAGACGCCGGC	GCTGAGCGAG	CTGATCGGTG	CTGCTGCCCG	CACTGGG CTG	4330
AAGCCCACCA	ATGACGCCGG	CGAAAACGAA	AAACCCGCC	GAGGCGGGGT	TTCTGACGCG	4390
GGTTGTGCGG	TCAGCTCAGA	ACGCCGGGAC	CACGGCGCCC	TTGTACTTTT	CCTCGATGAA	4450
CTGGCGTACT	TGCTCGCTGT	GCAGCGCGGC	AGCCAGTTTC	TGCATGGCAT	CGCTGTCCCT	4510
GTTGTCCGGA	CGGGCGACCA	GAATGTTCAC	GTATGGCGAG	TCGCTGCCCT	CGATCACCAG	4570
GGCGTCCTGG	GTCGGGTTCA	GCTTGGCTTC	CAGCGCGTAG	TTGGTGTGA	TCAGCGCCAG	4630
GTCGACCTGG	GTCAGCACGC	GCGGCAGAGT	CGCGGCTTCC	AGTCGCGGA	TCTTGATCTT	4690
CTTCGGGTTTC	TCGGCGATGT	CTTCGGCGTG	GCGGTGATGC	CGGCGCCGTC	CTTCAGACCG	4750
ATC						4753

Please replace the paragraph starting at page 9, line 31  
with the following amended paragraph.

Figure 1 shows an analysis of saccharides by thin-layer chromatography to which a reaction solution containing sonicated liquid from *Pseudomonas stutzeri* CJ38 and maltose solution was subjected. The symbols G.—G, M and T indicate glucose, maltose and trehalose, respectively. In the first lane of the gel shown in figure 1 is a control containing glucose, maltose and trehalose.